BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/084, 507_
Source: _OIPE_
Date Processed by STIC: _3-14-02_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlingtn, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary .

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/084,507_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos · was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering — use space characters, instead.

4____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" — sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) — (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) — <210> sequence id number
<400> sequence id number
000

9 ✓ Use of n's or Xaa's — Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) — Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response — scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" — resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means t copy file to floppy disk.

Does Not Comply
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING   DATE: 03/14/2002
PATENT APPLICATION: US/10/084,507   TIME: 12:24:35

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

```
  3 <110> APPLICANT: MUNROE, Donald G.
  4        KAMBOJ, Rajender
  5        PETERS, Diana
  6        KOOSHESH, Fatemeh
  7        VYAS, Tejal B.
  8        GUPTA, Ashwani K.
 10 <120> TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN
 11        INFLAMMATORY RESPONSE
 13 <130> FILE REFERENCE: 8074-8021
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/084,507
C--> 16 <141> CURRENT FILING DATE: 2002-02-28
 18 <150> PRIOR APPLICATION NUMBER: 60/109,885
 19 <151> PRIOR FILING DATE: 1998-11-25
 21 <150> PRIOR APPLICATION NUMBER: 60/080,610
 22 <151> PRIOR FILING DATE: 1998-04-03
 24 <150> PRIOR APPLICATION NUMBER: 60/070,185
 25 <151> PRIOR FILING DATE: 1997-12-30
 27 <160> NUMBER OF SEQ ID NOS: 25
 29 <170> SOFTWARE: PatentIn Ver. 2.1
```

ERRORED SEQUENCES

```
334 <210> SEQ ID NO: 17
335 <211> LENGTH: 353
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
339 <400> SEQUENCE: 17
340 Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
341  1               5                  10                  15
343 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
344              20                  25                  30
346 Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
347          35                  40                  45
349 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
350      50                  55                  60
352 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
353  65                  70                  75                  80
355 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
356              85                  90                  95
358 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
359             100                 105                 110
361 Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
```

RAW SEQUENCE LISTING   DATE: 03/14/2002
PATENT APPLICATION: US/10/084,507   TIME: 12:24:35

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

```
362           115                    120                    125
364 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
365           130                    135                    140
367 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
368 145                    150                    155                    160
370 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
371                    165                    170                    175
373 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
374                    180                    185                    190
376 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
377           195                    200                    205
379 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
380           210                    215                    220
382 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
383 225                    230                    235                    240
385 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
386                    245                    250                    255
388 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
389                    260                    265                    270
391 Xaa Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
392                    275                    280                    285
394 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
395           290                    295                    300
397 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Gly Thr
398 305                    310                    315                    320
400 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
401                    325                    330                    335
403 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
404                    340                    345                    350
406 Val
411 <210> SEQ ID NO: 18
412 <211> LENGTH: 1170
413 <212> TYPE: DNA
414 <213> ORGANISM: Homo sapiens
416 <400> SEQUENCE: 18
417 tttcggggta ccggggtcgt ccggagactc ggggtggtac ccgtcgaaca tgagcctcat 60
418 ggacttgggg ttgttccagg tccttgtgat attaatatgg ttcctctgcg acctttgcgt 120
419 cctctgctgg agggcggtcc accggagccg gaagtagcag taggagacaa cgcggtaaca 180
420 ccaccttttg gaagaccacg agtaacgcca ccgggctttg tcgttcaagg tgagccgtta 240
421 catggacaaa gacccgttgg accggcggag gctagatgac cgtccgcacc ggaagcatcg 300
422 gttatggaac gagagaccga gacagtgcga ctccgactgc ggacacgtca ccaaacgggc 360
423 cctcccgaga cggaagtagt gcgagagccg gagacagaag tcggaggacc ggtagcggta 420
424 actcgcggtg caccggtaac ggttccagtt cgacataccg tcgctgttct cgacggcgta 480
425 cgaagacgag tagccccgga gcaccgagta gagcgaccag gagccaccgg acgggtagga 540
426 accgaccttg acggacccgg tggagctccg gacgaggtga caggacggag agatgcggtt 600
427 cgtaatacac gacacgcacc actggtagaa gaggtagtag gacaaccggt agcaccggga 660
428 catgcacgcg tagatgacgc accaggcgag ttcggtgcga ctgtaccggc ggggcgtctg 720
429 cgatcgggac gagttctgcc agtggtagca cgatccgcag aaatagcaga cgaccgacgg 780
430 gcggaagtcg taggaggaag acctgatacg gacagggcag gtgaggacgg gctaggagat 840
```

E--> 391 (Xaa)

All 'Xaa' must have feature with numeric identifiers <2207 - <2237. See Item #9 on ERROR SUMMARY SHEET.

RAW SEQUENCE LISTING   DATE: 03/14/2002
PATENT APPLICATION: US/10/084,507   TIME: 12:24:35

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

```
       431 gtttcgggtg atgraaaagc ggcagaggtg ggacttaagg gacgagttgg ggcagtagat 900
E-->   432 gtgcaccgcg tcggccctgg acgccgccct ccacgaagcc ggcgacgtna cgaccgccgg 960
       433 cccccacccc cacgttcctg cctccgcccc gccctggggc ccggtggtgg aggacggtga 1020
       434 ggcgtcgagg tcgagggacc tctccccgta cgtgtacggg tgcagtgggt gaaaagacct 1080
       435 cccgttgtgc caccagactc ccaccccccac ctggttgttg gtccggtccc gtatccccaa 1140
       436 gtacctttcc ggtgacccac tggggtttat                                  1170
       742 <210> SEQ ID NO: 25
       743 <211> LENGTH: 1056
       744 <212> TYPE: DNA
       745 <213> ORGANISM: Homo sapiens
       747 <400> SEQUENCE: 25
       748 taccagtagt acccggtcac gatgatgttg ctctggtagc cgaagaagat attgttgtca 60
       749 ccgtttctcg agtcgagggt gaccgccggg ttcctacacc agcaccaccg tgaccccgac 120
       750 tggcagtcgc acgaccacga cgactggtta gacgaccagt atcgtcggta gcggaggttg 180
       751 gcggcgaagg tggtcgggta gatgatggac gagccgttag accggcgccg actggagaag 240
       752 cgcccgcacc ggatggagaa ggagtacaag gtgtgaccag gggcgtgtcg ggctgaaagt 300
       753 gaactcccga ccaaggacgc cgtcccgaac gacctgtgtt cggagtgacg cagccaccgg 360
       754 tgtgacgacc ggtagcggca cctcgccgtg gcgtcacact accggcacgt cgacgtgtcg 420
       755 gcggacgggg caccggcgca ccagtacgag taacacccgc acacccaccg acgggacccg 480
       756 gaccccgacg acggacgggt gaggaccgtg acggagacac gggacctggc gacgagtgcg 540
       757 taccgtgggg acgagtcggc gaggataaac cggcagaccc gagacagctc ggacgaacag 600
       758 aaggacgagt accaccgaca catgtgggcg taaaagaaga tgcacgccgc cgctcacgtc 660
       759 gcgtaccgtc tcgtacagtc gacggtgggg gcgatggctc tctggtgcga gtcggaccag 720
       760 ttctgacaac agtagtagga cccccgcaag caccagacga cctgtggtcc ggtccaccat 780
       761 gacgaggacc taccaaatcc gacactcagg acgttacagg accgacatct tttcatgaag 840
       762 gatgacgacc ggctccggtt gagtgaccag ttacgacgac acatgagaac ggctctacga 900
       763 ctctacgcgg cgtggaaggc ggcggaagag acgacgcgca cggaggcggt caggtgggcg 960
       764 ctcagacagg tgatatgtag gagacgggtc cctccacggt cgtgagcgta gtacgaaggg 1020
       765 ctcttgccgg tgggtgacta cctgaggtgg gaaatc                           1056
E-->   771 (2)
```

see page 2
Message same
for 'n'.

remove extra g material at end of file.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002
TIME: 12:24:36

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:308 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:391 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:432 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:1056 SEQ:25